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[1-¹⁴C]-isopentenyl diphosphate (1 Ci/mol) 25 nmol
 Allylic diphosphate (geranyl diphosphate) 25 nmol
 Potassium phosphate buffer (pH 5.8) 10 mM
 MgCl₂ 5 mM

Enzyme solution 100 µg

H₂O to make 200 µl

After the reaction is over, 200 µl of saturated NaCl was added to the reaction solution and 1 ml of water-saturated butanol was added thereto, which was then agitated, centrifuged, and separated into two phases. To 800 µl of the butanol layer obtained was added 3 ml of a liquid scintillator and then the radioactivity was measured by the scintillation counter. The result is shown in FIG. 2.

The mutant prenyl diphosphate synthase has exhibited a thermo stability which is equal to that of the native geranylgeranyl diphosphate synthase, and is higher than that of the farnesyl diphosphate synthase derived from *Bacillus stearothermophilus*.

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The solvent is evaporated from the remainder of the butanol layer by purging nitrogen gas thereto while heating the layer in order to concentrate to a volume of about 0.5 ml. To the concentrate were added 2 ml of methanol and one ml of potato acid phosphatase solution (2 mg/ml potato acid phosphatase, 0.5 M sodium acetate (pH 4.7)) to effect the dephosphorylation reaction at 37° C. Subsequently the dephosphorylated reaction product was extracted with 3 ml of n-pentane.

This was concentrated by evaporating the solvent by purging nitrogen gas thereto, which was then analyzed by TLC (reverse phase TLC plate: LKC18 (Whatman), development solvent: acetone/water=9/1). The developed dephosphorylated reaction product was analyzed by the Bio Image Analyzer BAS2000 (Fuji Photo Film) to determine the location of radioactivity. The result when geranyl diphosphate was used as the allylic substrate is shown in FIG. 3.

The reaction product of the mutant prenyl diphosphate synthase was shown to be a farnesyl diphosphate.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 14

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sulfolobus acidocaldarius*
 (B) STRAIN: ATCC 33909

(ix) FEATURE:

- (A) NAME/KEY: Asp-rich domain
 (B) LOCATION: 82-86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Ser Tyr Phe Asp Asn Tyr Phe Asn Glu Ile Val Asn Ser Val Asn
      5              10              15

Asp Ile Ile Lys Ser Tyr Ile Ser Gly Asp Val Pro Lys Leu Tyr Glu
      20              25              30

Ala Ser Tyr His Leu Phe Thr Ser Gly Gly Lys Arg Leu Arg Pro Leu
      35              40              45

Ile Leu Thr Ile Ser Ser Asp Leu Phe Gly Gly Gln Arg Glu Arg Ala
      50              55              60

Tyr Tyr Ala Gly Ala Ala Ile Glu Val Leu His Thr Phe Thr Leu Val
      65              70              75              80

His Asp Asp Ile Met Asp Gln Asp Asn Ile Arg Arg Gly Leu Pro Thr
      85              90              95

Val His Val Lys Tyr Gly Leu Pro Leu Ala Ile Leu Ala Gly Asp Leu
      100             105             110

Leu His Ala Lys Ala Phe Gln Leu Leu Thr Gln Ala Leu Arg Gly Leu
      115             120             125

Pro Ser Glu Thr Ile Ile Lys Ala Phe Asp Ile Phe Thr Arg Ser Ile
      130             135             140

Ile Ile Ile Ser Glu Gly Gln Ala Val Asp Met Glu Phe Glu Asp Arg

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-continued

AAGACTATAC TTGTAATAAA AACACTGGAG CTTTGTAAG AGGACGAGAA GAAGATTGTC 780
 CTAAAGGCGT TAGGTAATAA GTCAGCCTCA AAAGAAGAA TAATGAGCTC AGCAGATATA 840
 ATTAAGAAAT ACTCTTTAGA TTATGCATAC AATTTAGCAG AGAAATATTA TAAAAATGCT 900
 ATAGACTCTT TAAATCAAGT CTCTCTAAG AGTGATATAC CTGGAAAGGC TTTAAATAT 960
 CTAGCTGAAT TTACGATAAG AAGGAGAAAA TAA 993

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATACITTTT TCCTTGTGGC TGATGATATC ATGGATC 37

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATACITTTT TCCTTGTGCT TGATGATATC ATGGATC 37

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATACTTATT TCCTTGTGCT TGATGATATC ATGGATC 37

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATACTTATT TCCTTGTGGC TGATGATATC ATGGATC 37

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA